

Substitute_Sequence_Listing_CRF.txt
SEQUENCE LISTING

<110> ZENSUN(SHANGHAI)SCIENCE AND TECHNOLOGY LIMITED
Zhou, Mingdong

<120> ERBB3 BASED METHODS AND COMPOSITIONS FOR
TREATING NEOPLASMS

<130> 11748-006-999

<140> 10/516,759
<141> 2004-12-02

<150> PCT/CN03/00217
<151> 2003-03-26

<150> CH 02116259
<151> 2002-03-26

<160> 17

<170> FastSEQ for windows Version 4.0

<210> 1
<211> 1342
<212> PRT
<213> Homo sapiens

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20 25 30
Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
35 40 45
Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60
Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65 70 75 80
Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
85 90 95
Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100 105 110
Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115 120 125
His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
130 135 140
Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145 150 155 160
Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
165 170 175
Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
180 185 190
Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
195 200 205
Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
210 215 220
Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
225 230 235 240
Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
245 250 255
Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
260 265 270

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Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
275 280 285
Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
290 295 300
Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305 310 315 320
Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
325 330 335
Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
340 345 350
Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
355 360 365
Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
370 375 380
Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
385 390 395 400
Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
405 410 415
Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
420 425 430
Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
435 440 445
Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
450 455 460
His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
465 470 475 480
Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
485 490 495
Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
500 505 510
Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
515 520 525
Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
530 535 540
His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
545 550 555 560
Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
565 570 575
Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
580 585 590
Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
595 600 605
Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
610 615 620
Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
625 630 635 640
His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
645 650 655
Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
660 665 670
Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
675 680 685
Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
690 695 700
Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
705 710 715 720
Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
725 730 735
Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
740 745 750
Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
755 760 765
Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln

Substitute_Sequence_Listing_CRF.txt

770	775	780
Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser	Leu Leu Asp His Val Arg	
785	790	795
Gln His Arg Gly Ala Leu Gly Pro Gln Leu	Leu Leu Asn Trp Gly Val	800
805	810	815
Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu	Glu His Gly Met Val His	
820	825	830
Arg Asn Leu Ala Ala Arg Asn Val Leu Leu	Lys Ser Pro Ser Gln Val	
835	840	845
Gln Val Ala Asp Phe Gly Val Ala Asp Leu	Leu Pro Pro Asp Asp Lys	
850	855	860
Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro	Ile Lys Trp Met Ala Leu	
865	870	875
Glu Ser Ile His Phe Gly Lys Tyr Thr His	Gln Ser Asp Val Trp Ser	
885	890	895
Tyr Gly Val Thr Val Trp Glu Leu Met Thr	Phe Gly Ala Glu Pro Tyr	
900	905	910
Ala Gly Leu Arg Leu Ala Glu Val Pro Asp	Leu Leu Glu Lys Gly Glu	
915	920	925
Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile	Asp Val Tyr Met Val Met	
930	935	940
Val Lys Cys Trp Met Ile Asp Glu Asn Ile	Arg Pro Thr Phe Lys Glu	
945	950	955
Leu Ala Asn Glu Phe Thr Arg Met Ala Arg	Asp Pro Pro Arg Tyr Leu	
965	970	975
Val Ile Lys Arg Glu Ser Gly Pro Gly Ile	Ala Pro Gly Pro Glu Pro	
980	985	990
His Gly Leu Thr Asn Lys Lys Leu Glu Glu	Val Glu Leu Glu Pro Glu	
995	1000	1005
Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu	Glu Asp Asn Leu Ala Thr	
1010	1015	1020
Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro	Val Gly Thr Leu Asn Arg	
1025	1030	1035
Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro	Ser Ser Gly Tyr Met Pro	
1045	1050	1055
Met Asn Gln Gly Asn Leu Gly Glu Ser Cys	Gln Glu Ser Ala Val Ser	
1060	1065	1070
Gly Ser Ser Glu Arg Cys Pro Arg Pro Val	Ser Leu His Pro Met Pro	
1075	1080	1085
Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu	Gly His Val Thr Gly Ser	
1090	1095	1100
Glu Ala Glu Leu Gln Glu Lys Val Ser Met	Cys Arg Ser Arg Ser Arg	
1105	1110	1115
Ser Arg Ser Pro Arg Pro Arg Gly Asp Ser	Ala Tyr His Ser Gln Arg	
1125	1130	1135
His Ser Leu Leu Thr Pro Val Thr Pro Leu	Ser Pro Pro Gly Leu Glu	
1140	1145	1150
Glu Glu Asp Val Asn Gly Tyr Val Met Pro	Asp Thr His Leu Lys Gly	
1155	1160	1165
Thr Pro Ser Ser Arg Glu Gly Thr Leu Ser	Ser Val Gly Leu Ser Ser	
1170	1175	1180
Val Leu Gly Thr Glu Glu Glu Asp Glu	Glu Tyr Glu Tyr Met	
1185	1190	1195
Asn Arg Arg Arg His Ser Pro Pro His Pro	Pro Arg Pro Ser Ser	
1205	1210	1215
Leu Glu Glu Leu Gly Tyr Glu Tyr Met Asp	Val Gly Ser Asp Leu Ser	
1220	1225	1230
Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro	Leu His Pro Val Pro Ile	
1235	1240	1245
Met Pro Thr Ala Gly Thr Thr Pro Asp Glu	Asp Tyr Glu Tyr Met Asn	
1250	1255	1260
Arg Gln Arg Asp Gly Gly Pro Gly Gly Asp	Tyr Ala Ala Met Gly	
1265	1270	1275
		1280

Substitute_Sequence_Listing_CRF.txt

Ala	Cys	Pro	Ala	Ser	Glu	Gln	Gly	Tyr	Glu	Glu	Met	Arg	Ala	Phe	Gln
					1285				1290						1295
Gly	Pro	Gly	His	Gln	Ala	Pro	His	Val	His	Tyr	Ala	Arg	Leu	Lys	Thr
					1300				1305						1310
Leu	Arg	Ser	Leu	Glu	Ala	Thr	Asp	Ser	Ala	Phe	Asp	Asn	Pro	Asp	Tyr
					1315				1320						1325
Trp	His	Ser	Arg	Leu	Phe	Pro	Lys	Ala	Asn	Ala	Gly	Arg	Thr		
					1330				1335						1340

<210> 2
<211> 640
<212> PRT
<213> Homo sapiens

<400> 2
Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
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Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
20 25 30
Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
35 40 45
Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60
Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65 70 75 80
Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
85 90 95
Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
100 105 110
Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
115 120 125
His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
130 135 140
Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145 150 155 160
Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
165 170 175
Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
180 185 190
Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
195 200 205
Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
210 215 220
Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
225 230 235 240
Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
245 250 255
Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
260 265 270
Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
275 280 285
Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
290 295 300
Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305 310 315 320
Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
325 330 335
Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
340 345 350
Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
355 360 365
Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu

Substitute_Sequence_Listing_CRF.txt

370	Asn Val Phe Arg Thr Val	375	Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln	380
385	390	395	400	
Ser Trp Pro Pro His Met His Asn Phe Ser Val	405	410	Phe Ser Asn Leu Thr	415
Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser	420	425	Leu Leu Ile	430
Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser	435	440	Leu Lys Glu	445
Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg	450	455	Gln Leu Cys Tyr	460
His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro	465	470	Thr Glu	480
Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys	485	490	Val Ala Glu	495
Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys	500	505	Trp Gly Pro	510
Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg	515	520	Gly Gly Val	525
Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg	530	535	Glu Phe Ala	540
His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln	545	550	Pro Met Glu	560
Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys	565	570	Ala Gln Cys	575
Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys	580	585	Pro His Gly	590
Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp	595	600	Val Gln Asn	605
Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys	610	615	Lys Gly Pro	620
Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile	625	630	Gly Lys Thr	640

<210> 3
<211> 190
<212> PRT
<213> Homo sapiens

<400> 3

Met Arg Ala Asn Asp Ala Leu Gln Val	1	5	Leu Gly Leu Leu Phe Ser Leu	10	15
Ala Arg Gly Ser Glu Val Gly Asn Ser	20	25	Gln Ala Val Cys Pro Gly Thr	30	
Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn	35	40	Gln Tyr Gln Thr	45	
Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val	50	55	Met Gly Asn Leu Glu	60	
Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser	65	70	Phe Leu Gln Trp Ile	75	80
Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn	85	90	Glu Phe Ser Thr	95	
Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr	100	105	Gln Val Tyr Asp	110	
Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn	115	120	Thr Asn Ser Ser	125	
His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu	130	135	Thr Glu Ile Leu Ser	140	
Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys	145	150	His Met Asp Thr	155	160
Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala	165	170	Glu Ile Val Val	175	

Substitute_Sequence_Listing_CRF.txt

Lys	Asp	Asn	Gly	Arg	Ser	Cys	Pro	Pro	Cys	His	Glu	Val	Cys
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<210> 4

<211> 1914

<212> DNA

<213> Homo sapiens

<400> 4

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gctgagaacc	aataccagac	actgtacaag	ctctacgaga	ggtgtgaggt	ggtgatgggg	180
aacctgaga	ttgtgctcac	gggacacaat	gccgacctct	ccttcctgca	gtggattcga	240
gaagtgacag	gctatgtct	cgtgccatg	aatgaattct	ctactctacc	attgccaac	300
ctccgcgtgg	tgcgaggag	ccaggtctac	gatgggaagt	ttgccatctt	cgtcatgtt	360
aactataaca	ccaactccag	ccacgctctg	cgccagctcc	gctgactca	gctcaccgag	420
attctgtcag	ggggtgttta	tattgagaag	aacgataagc	tttgtcacat	ggacacaatt	480
gactggaggg	acatcgtgag	ggaccgagat	gctgagatag	tggtaagga	caatggcaga	540
agctgtcccc	cctgtcatga	ggtttgcaag	gggcgatgt	ggggtctgg	atcagaagac	600
tgccagacat	tgaccaagac	catctgtct	cctcagtgta	atggtcactg	ctttggccc	660
aacccaacc	agtgtgcga	tgatgagtgt	gccgggggt	gctcaggccc	tcaggacaca	720
gactgttttgc	cctgcccggca	cttcaatgac	agtggagct	gtgttacctcg	ctgtccacag	780
cctctgtct	acaacaagct	aacttccag	cttgaaccca	atccccacac	caagtatcag	840
tatggaggag	tttggtagc	cagctgtccc	cataactttg	tggtgatca	aacatcctgt	900
gtcaggccc	gtcctcctga	caagatggaa	gtagataaaa	atgggctcaa	gatgtgtgag	960
ccttgggg	gactatgtcc	caaagcctgt	gagggaaacag	gctctggag	ccgcttccag	1020
actgtggact	cgagcaacat	tgatggattt	gtgaactgca	ccaagatct	gggcaacctg	1080
gactttctga	tcaccggcct	caatggagac	ccctggcaca	agatccctgc	cctggaccca	1140
gagaagctca	atgtcttccg	gacagtaacgg	gagatcacag	gttacctgaa	catccagtcc	1200
tggccccc	acatgcacaa	tttcaatttgc	ttttccaattt	tgacaaccat	tggaggcaga	1260
agccttatac	accggggcctt	ctcattgttg	atcatgaaga	acttgaatgt	cacatctctg	1320
ggcttccgat	ccctgaagga	aattagtgt	gggcgtatct	atataagtgc	caataggcag	1380
ctctgttacc	accactcttt	gaactggacc	aagggtcttc	ggggcctac	ggaagagcga	1440
ctagacatca	agcataatcg	gccgcgcaga	gactgcgtgg	cagagggcaa	agtgtgtgac	1500
ccactgtgt	cctctgggg	atgttggggc	ccaggccctg	gtcaagtgtt	gtcctgtcg	1560
aattatagcc	gaggagggtgt	ctgtgtgacc	cactgcaact	tttcaatgg	ggagccctcg	1620
gaatttgc	atgaggccg	atgttctcc	tgccaccgg	aatgccaacc	catggagggc	1680
actgcacat	gcaatggc	gggcgtctgt	acttgcgtc	aatgtccca	ttttcgagat	1740
ggcccccact	gtgtgagcag	ctgccccat	ggagtcctag	gtgccaagg	cccaatctac	1800
aagtacccag	atgttcagaa	tgaatgtcg	ccctgccat	agaactgcac	ccaggggtgt	1860
aaaggaccag	agcttcaaga	ctgttttagga	caaacactgg	tgctgatcg	caaa	1914

<210> 5

<211> 475

<212> DNA

<213> Homo sapiens

<400> 5

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agacactgt	caagctctac	gagaggtgt	agggtggat	gggaaacctt	gagattgtgc	120
tcacggaca	caatgccac	ctctccttcc	tgcagtgtat	tcgagaagtg	acaggctatg	180
tcctcggtgc	catgaatgaa	ttctctactc	taccattgcc	caacctccgc	gtggtgcgag	240
ggaccggat	ctacgatgg	aagtttgc	tcttcgtcat	gttgaactat	aacaccaact	300
ccagccacgc	tctgcgccc	ctccgcttga	ctcagctcac	cgagattctg	tcaggggggt	360
tttatattga	gaagaacgt	aagctttgtc	acatggacac	aattgactgg	agggacatcg	420
tgaggaccg	agatgctgag	atagtggtga	aggacaatgg	cagaagctga	ctcg	475

<210> 6

<211> 19

<212> DNA

<213> Artificial Sequence

Substitute_Sequence_Listing_CRF.txt

<220>		
<223> Primer		
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tctgcggagt catgagggc		19
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<211> 48		
<212> DNA		
<213> Artificial Sequence		
<220>		
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<210> 8		
<211> 16		
<212> DNA		
<213> Artificial Sequence		
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<223> Primer		
<400> 8		
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<210> 9		
<211> 15		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
<400> 9		
gacgacgacg acaag		15
<210> 10		
<211> 16		
<212> DNA		
<213> Artificial Sequence		
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<400> 10		
gccatggctg atatcg		16
<210> 11		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Primer		
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gcaccaccac caccaccact gag		23
<210> 12		
<211> 28		

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 12

tggccatgga catcaagcat aatcgccc

28

<210> 13

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 13

gaaagactta cccctcggag agctcgtg

28

<210> 14

<211> 89

<212> PRT

<213> Homo sapiens

<400> 14

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15
Ala Gln Pro Ala Met Ala Met Asp Ile Lys His Asn Arg Pro Arg Arg
20 25 30
Asp Cys Val Ala Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly
35 40 45
Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr
50 55 60
Ser Arg Gly Gly Val Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu
65 70 75 80
Pro Leu Glu His His His His His
85

<210> 15

<211> 456

<212> DNA

<213> Homo sapiens

<400> 15

atggtttgtg tagccagctg tccccataac tttgtggtg atcaaacatc ctgtgtcagg 60
gcctgtcctc ctgacaagat ggaagttagat aaaaatggc tcaagatgtg tgagccttgt 120
gggggactat gtcccaaagc ctgtgaggga acaggctctg ggagccgctt ccagactgtg 180
gactcgagca acattgtatgg atttgtgaac tgcaccaaga tcctgggcaa cctggacttt 240
ctgatcaccc gcctcaatgg agaccctgg cacaagatcc ctgccctgga cccagagaag 300
ctcaatgtct tccggacagt acgggagatc acaggttacc tgaacatcca gtcctggccg 360
ccccacatgc acaacttcag tggggatcc aatttgacaa ccattggagg cagaaagctt 420
gcggccgcac tcgagcacca ccaccaccac cactga 456

<210> 16

<211> 151

<212> PRT

<213> Homo sapiens

<400> 16

Met Val Cys Val Ala Ser Cys Pro His Asn Phe Val Val Asp Gln Thr
1 5 10 15

Substitute_Sequence_Listing_CRF.txt

Ser Cys Val Arg Ala Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn
20 25 30
Gly Leu Lys Met Cys Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys
35 40 45
Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn
50 55 60
Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe
65 70 75 80
Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu
85 90 95
Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
100 105 110
Tyr Leu Asn Ile Gln Ser Trp Pro Pro His Met His Asn Phe Ser Val
115 120 125
Phe Ser Asn Leu Thr Thr Ile Gly Gly Arg Ser Lys Leu Ala Ala Ala
130 135 140
Leu Glu His His His His
145 150

<210> 17

<211> 270

<212> DNA

<213> Homo sapiens

<400> 17

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tgtgaccac tgtgctccctc tggggatgc tggggccca gcccgttca gtgcttgc 180
tgtcgaattt atagccgagg aggtgtctgt gtgaccact gcaactttct gaatggggag 240
cccctcgagc accaccacca ccaccactga 270